Serial No. 10/080,114 TC/A.U. 1638

Amendments to the Specification:

Please replace the paragraph beginning on page 9, beginning at line 20, with the following amended paragraph:

Figure 8. Figures 8a and 8b. Multiple alignment of maize sucrose synthase amino acid sequences.

Please replace the paragraph beginning on page 9, beginning at line 23, with the following amended paragraph:

Figure 9. Figures 9a - 9f. Multiple alignment of maize sucrose synthase polynucleotides.

Please replace the paragraph beginning on page 71, beginning at line 24, with the following amended paragraph:

Please replace the paragraph beginning on page 72, beginning at line 7, with the following amended paragraph:

Gene identities can be determined by conducting BLAST (Basic Local Alignment Search Tool; Altschul, S. F., et al., (1993) J. Mol. Biol. 215:403-410; see also the World Wide Web at www. ncbi.nlm.nih.gov/BLAST/) searches under default parameters for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from

Serial No. 10/080,114 TC/A.U. 1638

the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences are analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm. The DNA sequences are translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish, W. and States, D. J. Nature Genetics 3:266-272 (1993)) provided by the NCBI. In some cases, the sequencing data from two or more clones containing overlapping segments of DNA are used to construct contiguous DNA sequences.